



DSI10402.ST25.txt

SEQUENCE LISTING

<110> Cosenza, Lawrence W.
<120> SACROMASTIGOPHORIC THERAPEUTIC AGENT DELIVERY SYSTEM
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<140> US 10/735,203
<141> 2003-12-12
<150> US 60/433,269
<151> 2002-12-13
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<220>
<223> Primer for echovirus 1 VP3 protein
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<223> Primer for echovirus 1 VP3 protein

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<210> 10
<211> 39
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<220>
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<400> 10
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<210> 11
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<220>
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<400> 18
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<210> 19
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<212> DNA
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<220>
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<210> 21
<211> 843
<212> DNA
<213> Echovirus 1

<220>
<221> gene
<222> (1)..(843)
<223> Native VP1 shell protein

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caggcagtac ctggtgatac catgcagact agacatgtga tcaacaatca cgtgagggtca 180
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gtggtcatta caagctcgca agatcagtct acatcacaaa accagaatgc accagtgcta	420
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agctggcaaa catccaccaa cccagtatc ttttgaccg aagggaacgc tccggcacgc	540
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acg	843

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<211> 783
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 <213> Echovirus 1

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 ctaatgataa taccctttgt gcctctggat ttcagcgcggt gtgcatccac atacgtgccc 720
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 <212> DNA
 <213> Artificial

<220>
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 actacgtata aaactggaaa tgtttactta cctacggttt gacatggaaa tcaccgtggt 360
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<222> (1)..(843)
<223> Native VP3 shell protein

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 <303> Mol. Biochem. Parasitol.
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<212> PRT
<213> Homo sapiens

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Maeda,N.
<302> No trypanosome lytic activity in the sera of mice producing human
<303> Mol. Biochem. Parasitol.
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35          40          45

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50          55          60

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 85 90 95
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 100 105 110
 Gly Ser Phe Pro Trp Gln Ala Lys Met Val Ser His His Asn Leu Thr
 115 120 125
 Thr Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys
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 Asn Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala
 145 150 155 160
 Pro Thr Leu Thr Leu Tyr Val Gly Lys Lys Gln Leu Val Glu Ile Glu
 165 170 175
 Lys Val Val Leu His Pro Asn Tyr His Gln Val Asp Ile Gly Leu Ile
 180 185 190
 Lys Leu Lys Gln Lys Val Leu Val Asn Glu Arg Val Met Pro Ile Cys
 195 200 205
 Leu Pro Ser Lys Asn Tyr Ala Glu Val Gly Arg Val Gly Tyr Val Ser
 210 215 220
 Gly Trp Gly Gln Ser Asp Asn Phe Lys Leu Thr Asp His Leu Lys Tyr
 225 230 235 240
 Val Met Leu Pro Val Ala Asp Gln Tyr Asp Cys Ile Thr His Tyr Glu
 245 250 255
 Gly Ser Thr Cys Pro Lys Trp Lys Ala Pro Lys Ser Pro Val Gly Val
 260 265 270
 Gln Pro Ile Leu Asn Glu His Thr Phe Cys Val Gly Met Ser Lys Tyr
 275 280 285
 Gln Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val His
 290 295 300
 Asp Leu Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp
 305 310 315 320

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Lys Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Lys Val Thr Ser
325 330 335

Ile Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn
340 345